



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165365

TO: Phuong Bui

Location: rem/

Art Unit: 1638

Sept 14, 2005

Case Serial Number: 10/734698

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

Interference

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 12, 2005, 21:01:33 ; Search time 835 Seconds
(without alignments)
3083.064 Million cell updates/sec

Title: US-10-734-698A-39

Perfect score: 2083

Sequence: 1 MATFTLFTSBSVNEGHPDKL.....GREDDPDTWEVVKPLKWEKA 392

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastcap -SURFIX=rnpbp -MINMATCH=0.1
-LOOPCUI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10734698.cgn 1 1 800 @runat.12092005.134909.27452
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Published Applications NA:
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
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 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
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 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
 - 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
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 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
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 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2083	100.0	1465	18	US-10-425-114-10164	Sequence 10164, A
2	2083	100.0	1485	20	US-10-734-698A-38	Sequence 38, Appl
3	2083	100.0	1485	21	US-10-917-602A-38	Sequence 38, Appl
4	2083	100.0	1496	18	US-10-425-114-11983	Sequence 11983, A
5	2083	100.0	1518	17	US-10-431-252-1	Sequence 1, Appli
6	2083	100.0	1855	18	US-10-424-599-77204	Sequence 77204, A
7	2074	99.6	1509	18	US-10-425-114-29554	Sequence 29554, A
8	2073	99.5	1342	18	US-10-425-114-8517	Sequence 8517, Ap
9	2073	99.5	1349	18	US-10-425-114-11199	Sequence 11199, A
10	2073	99.5	1349	18	US-10-425-114-11868	Sequence 11868, A
11	2073	99.5	1427	18	US-10-425-114-12787	Sequence 12787, A
12	2073	99.5	1456	18	US-10-425-114-8399	Sequence 8399, Ap
13	2073	99.5	1456	18	US-10-425-114-10701	Sequence 10701, A
14	2073	99.5	1458	18	US-10-425-114-8336	Sequence 8336, Ap
15	2073	99.5	1461	18	US-10-425-114-8325	Sequence 8325, Ap
16	2073	99.5	1461	18	US-10-425-114-11194	Sequence 11194, A
17	2073	99.5	1468	18	US-10-425-114-10273	Sequence 10273, A
18	2073	99.5	1488	18	US-10-425-114-7202	Sequence 7202, Ap
19	2073	99.5	1488	18	US-10-425-114-7368	Sequence 7368, Ap
20	2073	99.5	1494	18	US-10-425-114-10112	Sequence 10112, A
21	2073	99.5	1495	18	US-10-425-114-10262	Sequence 10262, A
22	2073	99.5	1505	18	US-10-425-114-11712	Sequence 11712, A
23	2073	99.5	1510	18	US-10-425-114-11050	Sequence 11050, A
24	2073	99.5	1514	18	US-10-425-114-8323	Sequence 8323, A
25	2073	99.5	1514	18	US-10-425-114-9591	Sequence 9591, Ap
26	2073	99.5	1514	18	US-10-425-114-10155	Sequence 10155, A
27	2073	99.5	1514	18	US-10-425-114-10248	Sequence 10248, A
28	2073	99.5	1515	18	US-10-425-114-8286	Sequence 8286, Ap
29	2073	99.5	1515	18	US-10-425-114-8296	Sequence 8296, Ap
30	2073	99.5	1515	18	US-10-425-114-9070	Sequence 9070, Ap
31	2073	99.5	1515	18	US-10-425-114-9087	Sequence 9087, Ap
32	2073	99.5	1515	18	US-10-425-114-9138	Sequence 9138, Ap
33	2073	99.5	1515	18	US-10-425-114-10041	Sequence 10041, A
34	2073	99.5	1515	18	US-10-425-114-11285	Sequence 11285, A
35	2073	99.5	1515	18	US-10-425-114-12737	Sequence 12737, A
36	2073	99.5	1515	18	US-10-425-114-12745	Sequence 12745, A
37	2073	99.5	1523	18	US-10-425-114-10819	Sequence 10819, A
38	2073	99.5	1529	18	US-10-425-114-10266	Sequence 10266, A
39	2073	99.5	1529	18	US-10-425-114-12664	Sequence 12664, A
40	2060	98.9	1835	18	US-10-424-599-77205	Sequence 77205, A
41	2054	98.6	1538	18	US-10-424-599-115395	Sequence 115395, A
42	2046	98.2	1436	18	US-10-424-599-77201	Sequence 77201, A
43	2040.5	98.0	1459	18	US-10-425-114-9680	Sequence 9680, Ap
44	1999	96.0	1470	18	US-10-425-114-13126	Sequence 13126, A
45	1999	96.0	1479	18	US-10-425-114-11151	Sequence 11151, A

ALIGNMENTS

RESULT 1

US-10-425-114-10164
; Sequence 10164, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10164
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700896469_FLI
US-10-425-114-10164

Alignment Scores:
Pred. No.:      2,51e-228      Length:      1465
Score:          2083.00        Matches:      392
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00%     Indels:      0
DB:               18         Gaps:       0

US-10-734-698A-39 (1-392) x US-10-425-114-10164 (1-1465)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 54 ATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGAAGAGGACACCCCTGACAGCTC 113
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 114 TGGCAGCAAAATCTCCGATGCTGCTCGAGCGCTTGCCTTGAACAGGACCCAGACGCAAG 173
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 174 GTTGCCTGGCAACATGSCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACACC 233
QY 61 LysAlaAsnValAspTyrGluLysIleValAlaArgAspThrCysArgAsnIleGlyPheVal 80
DB 234 AAGCCCAACGTTGACTACGAGAAGATCGTGCGTGACACCTTCGAGGAAACATCGGCTCGTC 293
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
DB 294 TCAAACGATGGGACTTCTGATGCTGACAACTGCAAGGTCCTTGTAACATTCAGCAGCAG 353
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 354 AGCCCTTGATATTGCCAGAGGTGTGACGCGCCACCTTACCAAAAGACCCGAGGAAATCGGT 413
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 414 GCTGGAGACACAGGCTCAGATGTTTGCTATGCCACGACGACCCCAAGATTGATGCCA 473
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 474 TTGAGTGCATGTTCTTCAACTAAACTCGGTGCTCGTCTCACCGAGGTTCCCAAGAACGGA 533
QY 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnAsp 180
DB 534 ACCTGCCCCATGGTTGAGGCGCTGATGGGAAGACCCCAAGTCACTGTTGAGTATTACAAATGAC 593
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 594 AACGGTGCCATGGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAACATGATGAG 653
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 654 ACTGTGACCAACGACCAAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 713
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 714 CCGGAGAAGTACTCTGATCAGAGACCAATTTTCCACTTGAACCCCTCTCGCCGTTTTGTC 773
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 774 ATTGAGAGTCCCTCACGGTGATGCTGCTCTCACCGGCGCAAGATCATCATCGATCTTAC 833
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
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DB 834 GGAGGATGGGCTGCTCATGTGGTGGTCCCTTCTCCGGGAAGGATCCCAAGGTTGAT 893
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
DB 894 AGGAGTGGTGTTCATTTGTGAGACAGGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCC 953
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 954 AGAAGTGTCATTTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTTGCTGCTCTT 1013
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1014 GTTGACACCTATGGCACCAGGATCCATGATAGGAGATTCTCAACATTTGTGAAGGAG 1073
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyValAsn 360
DB 1074 AACTTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1133
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1134 AACAGTTCTTGNAGACTGCTGCATATGCACACTTCGGCAGAGAGACCCCTGACTTCACA 1193
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1194 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAAGGCC 1229

RESULT 2
US-10-734-698A-38
; Sequence 38, Application US/10734698A
; Publication No. US20040209341A1
; GENERAL INFORMATION:
; APPLICANT: FALCO, SAVERIO CARL
; ALLEN, STEPHEN M.
; RAFALSKI, J. ANTONI
; HITZ, WILLIAM D.
; KINNEY, ANTHONY J.
; ABELL, LYNNE N.
; THORPE, CATHERINE J.
; TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,698A
; FILING DATE: 12-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,771
; FILING DATE: 6-Jun-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MAJARIAN, WILLIAM R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1485 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 254 AAGGCCAACGTTGACTACGAGAGAGATCGTGGCTGACACCTCGAGGACATCGGCTTCGTC 313
QY 81 SerAsnAspValGlyLeuAspAlaAspAenCysLysValLeuValAsnIleGluGln 100
DB 314 TCAACAGCATGGGACTTCATGCTGACAACTCGAAGTCTTTGTAACATTCAGCAGCAG 373
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluIleGly 120
DB 374 AGCCCTGATATTGCCAGAGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAATCGGT 433
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 434 GTTGGAGACAGGCTCAGATGTTTGGCTATGCCGAGCAAAACCCAGAAATTGATGCCA 493
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 494 TTGAGTCATGTTCTTGCAACTAAACTCGGTGCTCGTCTCACCGAGGTTCCGAAGAACGCA 553
QY 161 ThrCysProTrioLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 554 ACTCTGCCATGTTGAGGCTCTGAGGAAACCCCAAGTACTGTTGAGTATTACAAATGAC 613
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 614 AACGGTGCCATGGTTCAGTTGTTGCCACATGCTGCTTATCTCCACCACATGATGAG 673
QY 201 ThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIle 220
DB 674 ACTGTGACCAACGACGAAATTGACGTGACCTCAAGGAGCATGTGATCAAGCGGTGATC 733
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 734 CCGGAGAACTACTTGATGAGAAGACCAATTTCCACTTGAACCCCTCTGGCCGTTTGTGC 793
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 794 ATTGGAGTCTCTACGGTGATGCTGGTCTCACGGGCCGCAAGATCATCATGATCTTAC 853
QY 261 GlyGlyTrioGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 854 CGAGGATGGGTGCTCATGCTGGTGTGCTTCTCCGGGAGGATCCCAACCAAGGTTGAT 913
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 914 AGAGTGGGTGCTTACATTTGTGACAGGCTGTCTAAGAGCATTTGTGCAAGTGGACTAGCC 973
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 974 AGAAGGTGCATTTGTGCAAGTGTCTTATGTCATTTGGTGTGCCGAGCCTTTGTCTCTTT 1033
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1034 GTTGACACCTATGGCACCGGGAAGATCCATGATAAGGAGATTTCTCAACATTTGTGAAGGAG 1093
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyLys 360
DB 1094 AACTTTGATTTAGGCCCGGTATGATCTCCATCAACTTGTATCTCAAGAGGGGTGGGAAT 1153
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1154 AACAGGTTCTTGNAGACTGCTGCATATGACACTTCGGCAGAGAGACCTTCGACTTCACA 1213
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1214 TGGGAAGTGGTCAAGCCCCCTCAAGTGGGAGAGGCC 1249
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RESULT 4

US-10-425-114-11983

; Sequence 11983, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

```
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11983
; LENGTH: 1496
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701150545_FLI
US-10-425-114-11983
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Pred. No.: 2083.00 Matches: 392
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 18
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US-10-734-698A-39 (1-392) x US-10-425-114-11983 (1-1496)

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DB 86 ATGGCAGAGACATTCCTATTACCTCAGAGTCAGTGAAGGAGGACACCTCGACAAGCTC 145
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 146 TCGCACCAAAATCTCGATGCTGCTCGACGCTTGCTTGAACAGGACCCAGACAGCAAG 205
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 206 GTTGCTCTCGAAACATGACATGACCACTTAAGACCAACTTGGTTCATGGTCTTCGGAGAGATCACACC 265
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 266 AAGGCCAACGTTGACTACGAGAGAGATCGTGGCTGACACCTCGAGGAACATCGGCTTCGTC 325
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
DB 326 TCAAAACGATGTGGGACTTGTATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAG 385
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 386 AGCCCTGATATTGCCAGGGTGTGACGGCCACCTTACCAAAAGACCCGAGGAATTCGGT 445
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 446 GCTCGAGACCCAGGCTCACAATGTTGGCTATGCCAGGAGAGACCCAGAAATTGATGCCA 505
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 506 TTGAGTCTATGTTCTTGGCAACTTAAACTCGGTGCTCGTCTCACCGAGGTTTCGCAAGAACGGA 565
QY 161 ThrCysProTrioLeuAspProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 566 ACCTGCCCATGGTTGAGGCTTGATGGGAGAGACCCAGTACTGTTGAGTATTACAAATGAC 625
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 626 AACGGTGCCATGGTTCAGTTGCTGCTCCACTGCTGCTTATCTCCACCACATCATGATGAG 685
QY 201 ThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIle 220
DB 686 ACTGTGACCAACGAGAAATTCAGCTGACCTCAAGGAGGAGCATGTGATCAAGCCGGTGATC 745
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QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 746 CCGGAGAAGTACCTTGATGAGAACACCATTTTCACCTGAACCCCTCTGGCCGTTTGTGTC 805
QY 241 IleGlyClyProHisGlyAspAlaGlyLeuThrClyArgLysIleIleAspThrTyr 260
Db 806 ATTGGAGGTCTCACGGTGTATGCTGGTCTCACCGGCCGCAAGATCATCATCGATCTTAC 865
QY 261 GlyClyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 866 GGAGGATGGGGTGTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 925
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 926 AGGAGTGGTCTTACATTTGTGAGACAGCTGCTAAGAGCATTTGTGGCAAGTGGACTAGCC 985
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 986 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCGCGCTTTGTCTGCTTT 1045
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1046 GTTGACACCTATGGCACCGGAGATCCATGATGAAGAGATTCTCAACATTGTGAAGGAG 1105
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1106 AACTTTGATTTCAGGCCGCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1165
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1166 AACAGGTTCTTGAAGACTGTGTCATATGACACTTCGGCAGAGAGGACCCCTGACTTCACA 1225
QY 381 TrpGluValValLysProLeuLysTyrGluLysAla 392
Db 1226 TGGAAAGTGTCAAGCCCTCAAGTGGGAGAGGCC 1261

RESULT 5
US-10-431-252-1
; Sequence 1, Application US/10431252
; Publication No. US20030226166A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhongsen
; APPLICANT: Falco, S. Carl
; TITLE OF INVENTION: S-ADENOSYL-L-METHIONINE SYNTHETASE PROMOTER AND
; TITLE OF INVENTION: ITS USE IN EXPRESSION OF TRANSGENIC GENES IN PLANTS
; FILE REFERENCE: BB1205 US CIP
; CURRENT APPLICATION NUMBER: US/10/431,252
; PRIOR FILING DATE: 2003-05-07
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Glycine max
US-10-431-252-1

Alignment Scores:
Pred. No.: 2,64e-228 Length: 1518
Score: 2083.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-431-252-1 (1-1518)
QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
|||||
```

```
Db 74 ATGGCAGAGACATTCCTATTTCCTCAGAGTCAGTGAAACGAGGGACACCCCTGACAAGCTC 133
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGlnAspProAspSerLys 40
Db 134 TGGCAGCAAAATCTCCGATGCTGCTCTCGACGCTTGCCTTGAACAGAGACCCAGAGCAAG 193
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 194 GTTGCCTGCGAAACATGSCCAAGACCAACTTGGTTCATGCTCTTCGGAGAGATCACACC 253
QY 61 LysAlaAsnValAspTyrGluLysIleValAlaArgAspThrCysArgAsnIleGlyPheVal 80
Db 254 AAGGCCCAACGTTGACTTACGAGAAGATCGTGGTGACCTTCAGGAAACATCGGCTTCGTC 313
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 314 TCDAACGATGTGGGACTTGTATGCTGACAACTGCAAGTCTCTGTAAACATTGAGACGAG 373
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 374 AGCCCTGATATTGCCAGGGTGTGCACGGCCACCTTACCAGGAGACCCGAGGAAATCGGT 433
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 434 GCTGGAGACACAGGTCATGTTTGGCTATGCCACGACGAAACCCAGAAATTGATGCCA 493
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 494 TTGAGTCATGTTCTTGAACATAAAGTCTCGTCTCGTCTCACCGAGGTTCCGAGAAACGGA 553
QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 554 ACTCTGCCATGTGTAGGCTGATGGGAAACCCCAAGTGAAGTCTGTTGAGTATTACAAATGAC 613
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 614 AACGGTGCATGTGTTCCAGTCTGTGTCCACACTGTGCTTATCTCCACCCAAACATGATGAG 673
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 674 ACTGTGACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGTATC 733
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 734 CCGGAGAAGTACCTTGATGAGAACACATTTTCACCTTGAACCCCTCTGGCCGTTTGTGTC 793
QY 241 IleGlyClyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 794 ATTGAGGTCCTCACGGTGTATGCTGTCTCACCGCCGCAAGATCATCATCGATCTTAC 853
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 854 GGAGGATGGGGTGTCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 913
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 914 AGGAGTGGTGTCTTACATTGTGAGACAGGCTGTCTAAGAGCATTTGTGCAAGTGGACTAGCC 973
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 974 AGAAGTGCATTTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGGCTTGTCTGTCTTT 1033
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1034 GTTGACACCTATGGCACCGGAGATCCATGATAGGAGATTCTCAACATTGTGAAGGAG 1093
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1094 AACTTTGATTTTCAAGCCCGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGGAAT 1153
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1154 AACAGGTTCTTGAAGACTGCTCATATGACACTTCGGCAGAGAGACCCCTGACTTCACA 1213
```

QY 381 TrpGluValValysProLeuLysTrpGluLysAla 392
DB 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249

RESULT 6

US-10-424-599-77204
; Sequence 77204, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 77204
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40730C.1
US-10-424-599-77204

Alignment Scores:
Pred. No.: 3,5e-228 Length: 1855
Score: 2083.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-424-599-77204 (1-1855)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 140 ATGGCAGAGACATTTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTCGACAGCTC 199
QY 21 CysAspGlnPheSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 200 TGGGACCAAAATCTCCGATGCTGCTTCGACGCTTGCTTGAACAGACCCAGACAGCAAG 259
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluLeuThrThr 60
DB 260 GTTGCCTGGAAACATGCACCAAGACCAACTTTGGTCATGGTCTTCGAGAGATCACCACC 319
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 320 AAGGCCAACCGTTGACTACGAGAAGATCGTGGCGTGACCTGCAGGGAACATCGCTTCGTC 379
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
DB 380 TCAAACATGTGGGACTTGATGCTGACCACTGCAGGCTCTTGTAACATTGAGCAGCAG 439
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluLeuGly 120
DB 440 AGCCCTGATATTGCCCAGGCTGTCACGCGCACCTTACCAGGAGCCCGAGGAAATCGGT 499
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 500 GTTGGAGACACGGGTCAATGTTGGCTATGCGACGAGCAGACCCAGAAATGATGCCA 559
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 560 TTGAGTCATGTTCTTGCACATAAACTCGGTGCTCGTCTCACCGAGGTTCCGAGAACGGA 619
QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAsp 180
DB 620 ACCTGCCCCATGTTGAGGCTGTATGGGAGAGACCAAGTGAAGTCTGTTGAGTATTACAATGAC 679

QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuLysSerThrGlnHisAspGlu 200
DB 680 AACGGTGCCATGGTTCCAGTTTCGTTGTCACACTGTCTTATCTCCACCAACATGATGAG 739
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 740 ACTGTGACCAACGAGGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 799
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 800 CCGGAGAAAGTACCTTGTATGAGAGAACCAATTTTCCACTTGAACCCCTCTGGCGTTTGTG 859
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleLeuAspThrTyr 260
DB 860 ATTGGAGGTCTCTCAGGTGATGCTGTCTCACCGGCCGCAAGATCATCATCATGATCTTAC 919
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 920 GGAGGATGGGTGCTCATGTTGGTGGTCTTCTCCGGGAAGGATCCCAAGGTTGAT 979
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
DB 980 AGGAGTGGTGTCTTACATTTGTGAGACAGGCTGCTAAGAGCATTTGTGSCAAGTGGACTAGCC 1039
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 1040 AAGGTGCATTTGCAAGTGTCTTATGCCATTTGGTGTGCGGAGCCCTTGTCTGTCTTT 1099
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1100 GTTGACACCTATGGCAGCGGAGAGATCCATGATAGGAGATTCTCAACATTGTGAAGGAG 1159
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsn 360
DB 1160 AACTTTGATTTTCAGGCCCGGTATGATCTCTCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1219
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1220 AACAGGTTCTTGAAGACTGTGTCATATGACACTTTCGCGCAGAGAGACCTTGACTTCACA 1279
QY 381 TrpGluValValysProLeuLysTrpGluLysAla 392
DB 1280 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1315

RESULT 7
US-10-425-114-29554
; Sequence 29554, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29554
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMELMINSOY064D01_FLI
US-10-425-114-29554

Alignment Scores: 2,82e-227 Length: 1509
Pred. No.: 2074.00 Matches: 390
Score:

Percent Similarity: 99.74% Conservative: 1
Best Local Similarity: 99.49% Mismatches: 1
Query Match: 99.57% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-29554 (1-1509)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 89 ATGGCAGAGACATTCTCTATTACCTCAGAGTCGGTGAACGAGGACACCCCTGACAGCTC 148
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 149 TGGCAGCAAAATCTCCGATGCTGCTCTCGACGCTTGCCCTGAGCAGGACCCAGACAGCAA 208
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 209 GTTGCTCGCAACATGCACCAAAACCACTTGCTCATGTCTTCGGAGAAATCAGACC 268
Qy 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 269 AAGGCCAACGCTGACTACGAGAAGATAGTCGTGACACCTGCAGGAACATCGGCTTCGTC 328
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 329 TCAATGATGTGGACTGGATGCCACAACTGCAAGGTCTCTGCAACATTGAGCAGCAG 388
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 389 AGCCCTGATATTGCTCAGGCTGTACACGGCCACTTACCAAAAACCTTGAAGAAATTTGGT 448
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 449 GCTGGTGACGAGGTACATGTTTGGCTATGCCACTGATGAACCCCTGAAATTTGATGCCA 508
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 509 TTGAGCCATGTTCTTGCAACAAATCTCGTGTCTCACCAGGTTTCGCAAGAACGGT 568
Qy 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 569 ACTGCTGCTGGCTGAGCGCTGATGGGAACCCAAAGTACCCTTGAGTATTCAATGAC 628
Qy 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 629 AATGCTGCCAGGTTCGGTTCGTGTCCACACCGTCTAATCTCCACCCCAACAGCAGAG 688
Qy 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 689 ACTGTCAACCAATGACCAATGCTGTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 748
Qy 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 749 CCAGAGAAGTACCTTGATGAGAAGACCATTTTCCACTTGAAACCTTCAGGCCGCTTTTGC 808
Qy 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
Db 809 ATTGCTGGCCCTCATGCGATGCTGCTCACCAGCGCGCAAGATCATATCATCTAT 868
Qy 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 869 GGAGGATGGGTGCTCATGTGTGTGTGCTTTCCTCCGGGAAGACCCCTACCAAGTTGAT 928
Qy 281 ArgSerGlyValIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 929 AGAGTGTGCTTACATTGTGACAGCGCTGCTTAAGAGCATTTGCGCAAGTGCAGCTGCC 988
Qy 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 989 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCTCAGGCTTTGCTGTGTTT 1048
Qy 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340

Db 1049 GTTGACACCTATGGCACTGGGAAGATCCATGATTAAGAGATTCTCAACATTGTGAAGGAA 1108
Qy 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1109 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACTTGTATCTCAAGAGGGTGGAAAT 1168
Qy 361 AsnArgPheLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1169 AACAGGTTTTTGAAGACTGCTGCTATGGACACTTTTGAAGAGAGAGACCCCTGACTTCACA 1228
Qy 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1229 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1264

RESULT 8
US-10-425-114-8517
; Sequence 8517, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8517
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700757167_FLI
US-10-425-114-8517

Alignment Scores:
Pred. No.: 3 116-227 Length: 1342
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservatives: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8517 (1-1342)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 95 ATGGCAGAGACATTCTCTATTACCTCAGAGTCGGTGAACGAGGACACCTGACAGCTC 154
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 155 TGGCAGCAAAATCTCCGATGCTGCTCGACGCTTGCTCGAGCAGGACCCAGACAGCAA 214
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 215 GTTGCTCGCAACATGACCAACCAACTTGGTCTATGCTCTTCGGAGAAATCAGACC 274
Qy 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 275 AAGGCCAACGTTGACTACGAGAAGATAGTCGTGACACCTGCAAGGAACATCGGCTTCGTC 334
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 335 TCAATGATGTGGGACTGGATGCCACAACTGCAAGGTCTCTGCTCAACATTGAGCAGCAG 394
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 395 AGCCCTGATATTGCTCAGGCTGTACACGCCACCTTACCAAAAACCTTGAAGAAATTTGGT 454

```
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 455 GCTGGTGACAGGTCACATGTTGGCTATGCCACTGATGAACCCCTGATGATGCCA 514
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 515 TTGAGCCATGTTCTTGCAACAAACCTCGGTGCTCGTCTCACCGAGGTTGCAAGAAGCGT 574
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 575 ACCTGCCCTTGGCTGAGGCTGATGGGAAGACCCCAAGTAGCCGTTGAGTATTACAAATGAC 634
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 635 AATGGTGCCAGGGTTCCTATTGCTGACACCGCTGCTAATCTCCACCCACACAGCAG 694
QY 201 ThrValThrAsnAspGluLeuAlaAspLeuLysGluHisValIleLysProValIle 220
Db 695 ACTGTCAACCAATGACGAATGCTGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 754
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 755 CCAGAGAAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCCCTTCAGGCCGTTTGTG 814
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 815 AATGGTGCCCTCATGCGCATGCTGTCTCACCGGCCGCAAGATCATATCATCTACTTAT 874
QY 261 GlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 875 GGAGGATGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGACCTTACCAGGTTGAT 934
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 935 AGGAGTGGTGGCTTACATTGTGACAGGCTGCTAAGAGCATTTGTGCGCAAGTGGACTTGC 994
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 995 AGAAGTGCAATTGTGCAAGTGCTTATGCAATGGTGCTGCTGAGCCCTTGTCTGTGTTT 1054
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1055 GTTGACACCTATGGCACTGGGAAGATCCATGATGAAGAGATTCTCAACATTGTGAAGGAA 1114
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyLysAsn 360
Db 1115 AACTTTGATTTTTCAGGCTGCTGATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGAAT 1174
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1175 AACAGTTTTTGAAGACTGCTGCTATGACACTTTGGAGAGAGACCTGATCTTCA 1234
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1235 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1270
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RESULT 9

```
US-10-425-114-11199
; Sequence 11199, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(S3313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
```

```
; SEQ ID NO 11199
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701040251_FLI
US-10-425-114-11199
```

Alignment Scores:

Pred. No.:	3.13e-227	Length:	1349
Score:	2073.00	Matches:	389
Percent Similarity:	99.74%	Conservative:	2
Best Local Similarity:	99.23%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	18	Gaps:	0

US-10-734-698A-39 (1-392) x US-10-425-114-11199 (1-1349)

QY	1	MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu	20
Db	85	ATGGCAGACATTCCTATTATCTCAGAGTCGGTGAACGAGGGACACCTGACAGCTC	144
QY	21	CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys	40
Db	145	TGCGACCAAAATCTCCGATGCTGCTCGACGCTTGCCTCGAGCAGACCCACAGACAAA	204
QY	41	ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr	60
Db	205	GTTGCCCTGCGAAACATGACCAAAACCAACTTGGTTCATGGTCTTCGAGAAATACGACC	264
QY	61	LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal	80
Db	265	AAGGCCAACGTTGACTACGAGAGATAGTGGTGACACTGCGAGGAACATCGGCTTCGTC	324
QY	81	SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln	100
Db	325	TCAATATGATGTGGGACTGCGATGCCGACAACCTGCAAGGTCTCTCAACATTGAGCAGAG	384
QY	101	SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly	120
Db	385	AGCCCTTGATATTTGCTCAGGGGTGTACACGCCACCTTACCAAAAAACCTCGAAGAAATGGT	444
QY	121	AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro	140
Db	445	GCTGGTGACAGGGTCACATGTTTGGCTATGCCACTGATGAACCCCTGATGATGCCA	504
QY	141	LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly	160
Db	505	TTGAGCCATGTTCTTGCACAAAACTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACGGT	564
QY	161	ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp	180
Db	565	ACCTGCCCTTGGCTGAGGCCCTGATGGGAAGACCCCAAGTGACCGTTGAGTATTACAAATGAC	624
QY	181	AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu	200
Db	625	AATGGTGCCAGGGTTCCTATTTCGTGTACACACCGCTGCTAATCTCCACCCACACAGCAG	684
QY	201	ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle	220
Db	685	ACTGTCAACAAATGCGAATTCGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC	744
QY	221	ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal	240
Db	745	CCAGAGAAAGTACCTTGATGAGAAGACCAATTTTCCACTTGAACCCCTTCAGGCCGTTTGTG	804
QY	241	IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr	260
Db	805	ATTGGTGCCCTCATGGCGATGCTGCTCTCACCGGCCGCGAAGATCATTTATCGATCTTAT	864
QY	261	GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp	280
Db	865	GGAGGATGGGGTGTCTCATGGTGGTGGTCTTTTCTCCGGGAAGGACCTTACCAAGGTTGAT	924

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Qy 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 925 AGGAGTGGTCTTACATTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTTGCC 984
Qy 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 985 AGAAGGTGCATTGGCAATGGCAAGTGTCTTATGCCATTGGTGTGCTGAGCCCTTTGTCTGTGTTT 1044
Qy 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1045 GTTGACACCTATGGCACTGGAGATCCATGATGAAGAGATTCTCAACATTGTGAAGGAA 1104
Qy 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1105 AACTTTGATTTCAGCCCTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1164
Qy 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1165 AACAGGTTTTTGAAGACTGTGCTGCTATGAGACATTTTGAAGAGAGAGACCTGACTTCACA 1224
Qy 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1225 TGGGAAGTGTCTCAACCCCTCAAGTGGGAGAGGCC 1260

RESULT 10
US-10-425-114-11868
; Sequence 11868, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11868
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701137731_FLI
US-10-425-114-11868

Alignment Scores:
Pred. No.: 3,13e-227 Length: 1349
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-11868 (1-1349)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 89 ATGGCAGAGACATTCTCTATTACCTCAGAGTCGGTGAACGAGGGAACACCCCTGACAAAGCTC 148
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 149 TGGACACCAATCTCCGATGTGCTCTCGACGCTTGCCCTGAGCAGGACCCAGACAGCAAA 208
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 209 GTTGCCCTGGCAACATGCACCAAAACCACTTGGTCATGTCTTCGGAGAAATCAGACC 268
Qy 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
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Db 269 AAGGCCAACGTTGACTACGAGAAGATAGTGCCTGACACCTGCAGGAACATCGCTTCGTC 328
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 329 TCNAATGATGTGGACTGATGCCGACAACTGCAGAGTCTCTGTCACCAATTGAGCAGCAG 388
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 389 AGCCCTGATATTGCTCAGGGTGTACACGCCACCTTACCACAAAAACCTGAAGAAATGGT 448
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 449 GCTGSGTGCACCGGGTCACATGTTGGCTATGCCATGACCTGATGAACCCCTGAATTGATGCCA 508
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 509 TTGAGGCATGTTCTTGCACAAAACTCGGTGTCTGCTCACCAGGTTCCGCAAGACGGT 568
Qy 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 569 ACTGCGCCCTGGCTGAGGCTGATGGGAAGACCCAAAGTGACCGTTGAGTATTACAATGAC 628
Qy 181 AsnGlyAlaMetValProValArgValHisThrValIleIleSerThrGlnHisAspGlu 200
Db 629 AATGSGTCCAGGGTTCTTATTCGTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 688
Qy 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 689 ACTGTCCACCAATGACGAAATTCGTGCTGACCTCAAGAGCANTGTGATCAAGCCTGTGATC 748
Qy 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 749 CCAGAGAAGTACTTGTGATGAGAAGACCAATTTTCCACTTGAACCCCTTCAGGCCGTTTTGTC 808
Qy 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
Db 809 ATTGSGTGGCCCTCATGGCGATGCTGCTCACCGGCCGCAAGATCATTTATCGATACTTAT 868
Qy 261 GlyGlyTyrTrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 869 GGAGAGATGGGTGCTCATGTGTGTGTGCTTCTCCGGNAGGACCCCTACCAAGGTTGAT 928
Qy 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
Db 929 AGGAGTGGTGTCTTACATTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTTGCC 988
Qy 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 989 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGTGTGCTGAGCCCTTTGTCTGTGTTT 1048
Qy 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1049 GTTGACACCTATGGCACTGGGAAAGATCCATGATGAGAGATTCTCAACATTGTGAAGGAA 1108
Qy 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1109 AACTTTGATTTTCAGGCCCTGATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGAAT 1168
Qy 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1169 AACAGGTTTTTGAAGACTGTGCTCTATGGACACTTTTGAAGAGAGAGACCCCTGACTTCACA 1228
Qy 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1229 TGGGAAGTGTCTCAACCCCTCAAGTGGGAGAGGCC 1264

RESULT 11
US-10-425-114-12787
; Sequence 12787, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
```

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 12787
LENGTH: 1427
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701211701_FLI
US-10-425-114-12787

Alignment Scores:
Pred. No.: 3,39e-227 Length: 1427
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-12787 (1-1427)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 65 ATGGCAGAGACATTCTTATTTACCTCAGAGTGGTGAACGAGGACACCTTCACAAGCTC 124
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 125 TGGGACCAATCTCCGATGCTGCTCGACGCTTGCCTCGAGCAGGACCACAGACGCAA 184
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 185 GTTGCTCTGGAAACATGCACCAAAACCACTTGGTCAATGGTCTTCGGAGAAATCAGACC 244
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 245 AAGGCCAAGCTTGACTACGAGAAGATAGTGGTGACACCTGCAGGAAACATCGCTTCGTC 304
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
DB 305 TCAAAATGATGTGGGACTGGATGCCGACAACTGCAAGGTCTCTGTCACACATTGAGCAGCAG 364
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 365 AGCCCTGATATTGCTCAGGGGTGACAGGCCACCTTACCAGAAACCTGAGAAATTTGT 424
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 425 GCTGGTGACAGGGTCACATGTTTGGCTATGCCACTGATGAACCCCTGAATTGATGCCA 484
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 485 TTGAGCCATGTTCTTGCACAAACAACTCGGTGCTCGTCTCACCAGGAGTTGCAAGAACGCT 544
QY 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 545 ACCTGCCCTTGGCTGAGGCTGATGGGAAGACCAAGTACCGCTTGAGTATTACATGAC 604
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 605 AATGGTGCCAGGGTTCCTATTCTGTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 664
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 665 ACTGTACCAATGACGAAATTCGTGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 724

QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 725 CCAGAGAAGTACCTTGATGAGAGACCAATTTCCACTTGAACCTTTCAGGCGCTTTGTC 784
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 785 ATTGGTGGCCCTCATGCGGATGCTGTCTCACCGCCGCAAGATCATTCATGATCTTAT 844
QY 261 GlyGlyTyrGlyAlaHisGlyGlyValAlaPheSerGlyLysAspProThrLysValAsp 280
DB 845 GGAGGATGGGTGCTCATGGTGGTGGTCTTCTCCGGAAGGACCTTACCAAGGTTGAT 904
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 905 AGGAGTGGTGTACATTGTGAGACAGGCTGCTAGAGCATTTGTGCAAGTGGACTTGGC 964
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 965 AGAAGGTGCAATGTGCAAGTGTCTTATGCCATTGGTGGCTGAGCCTTTGTCTGTGTTT 1024
QY 321 ValAspThrTyrGlyThrClyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1025 GTTGACACCTATGGCAGCTGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAA 1084
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1085 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1144
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1145 AACAGGTTTTTCAAGACTGCTGCCCTATGGACACTTTTGAAGAGAGACCCCTGACTTCACA 1204
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1205 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAAGGCC 1240

RESULT 12
US-10-425-114-8399
Sequence 8399, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8399
LENGTH: 1456
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700751645_FLI
US-10-425-114-8399

Alignment Scores:
Pred. No.: 3,49e-227 Length: 1456
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8399 (1-1456)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
|||||

Db 90 ATGGCAGAGACATTCCTATTATTAAGCTGAGTGGTGAACGAGGGACACCCCTGACAAGCTC 149
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 150 TGGCAGCAAAATCTCCGATGCTGCTCGACGCTTGCTCGAGCAGGACCCAGACAGCAA 209
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 60
Db 210 GTTGCCTCGCAAAATGACCAAAACCACTTGCTGATGCTTTCGAGAGAAATCAAGACC 269
Qy 61 LysAlaAsnValAspTyrGluLysIleValLysAspThrCysArgAsnIleGlyPheVal 80
Db 270 AAGGCCAACGTTGACTACGAGAAGATAGTCGTCGACACCTGCAGGAACATCGGCTTCGTC 329
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 330 TCAATGATGTGGACTGGATGCCCAACTCGAAGTCTCTCAACATTGAGCAGCAG 389
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 390 AGCCCTGATATTGCTCAGGGTGTACACGGCCACCTTACCAGAAACCTGAAGAAATTTGGT 449
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 450 GCTGGTGACGAGGTCATGTTGGCTATGCCACCTGATGAACCCCTGAATTGATGCCA 509
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 510 TTGAGCCATGTTCTTGGCAACAACTCGGTGCTCGTCTCACCGAGGTTCCGCAAGACGGT 569
Qy 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 570 ACCTGCTGCTGGTGGCTGATGGAGAGACCAAGTGACCTGATCAAGCTGTGATC 629
Qy 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 630 AATGGTGGCCAGGGTCTCTATCTGTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 689
Qy 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 690 ACTGTACCANTGACGNAATGCTGTGACCTCAAGAGCATGTGATCAAGCTGTGATC 749
Qy 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 750 CCAGAGAAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCTTCAGGCCGCTTTTGTG 809
Qy 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 810 ATTGGTGGCCCTCATGGCGATGCTGGTCTCACCGCCGCAAGATCATTAATCGATCTTAT 869
Qy 261 GlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 870 GGAAGATGGGGTCTCATGGTGGTGGTCTTCTCCGGGAGACCCCTACCAAGTTGAT 929
Qy 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 930 AGCAGTGGTCTTACATGTTGAGACAGGCTGTCAAGAGCATTTGTGCAAGTGGACTTGGC 989
Qy 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 990 AGAAGGTGCATTGTGCAAGTGTCTATGCCATTGGTGTGCTCGAGCTTTGCTGTGTTT 1049
Qy 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1050 GTTGACACCTATGGCACTGGGAAGATCCATGATAGGAGATTTCTCAACATTGTGAAGGAA 1109
Qy 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1110 AACTTTGATTTACGGCTGATGATGATCTCCATCAACCTTGATCTCAAGAGGGGTGCAAT 1169
Qy 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1170 AACAGGTTTTTGAAGACTGCTGCTATGGACACTTTTGGAGAAGAACCCCTGACTTCA 1229

Qy 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1230 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAAGGCC 1265

RESULT 13

US-10-425-114-10701
; Sequence 10701, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10701
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700961178_FLI
US-10-425-114-10701

Alignment Scores:
Pred. No.: 3,49e-227 Length: 1456
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-10701 (1-1456)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 90 ATGGCAGAGACATTCCTATTATTAAGCTGAGTGGTGAACGAGGGACACCCCTGACAAGCTC 149
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 150 TGGCAGCAAAATCTCCGATGCTGCTCGACGCTTGCTCGAGCAGGACCCAGACAGCAA 209
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 60
Db 210 GTTGCCTCGCAAAATGACCAAAACCACTTGCTGATGCTTTCGAGAGAAATCAAGACC 269
Qy 61 LysAlaAsnValAspTyrGluLysIleValLysAspThrCysArgAsnIleGlyPheVal 80
Db 270 AAGGCCAACGTTGACTACGAGAAGATAGTCGTCGACACCTGCAGGAACATCGGCTTCGTC 329
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 330 TCAATGATGTGGACTGGATGCCCAACTCGAAGTCTCTCAACATTGAGCAGCAG 389
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 390 AGCCCTGATATTGCTCAGGGTGTACACGGCCACCTTACCAGAAACCTGAAGAAATTTGGT 449
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 450 GCTGGTGACGAGGTCATGTTGGCTATGCCACCTGATGAACCCCTGAATTGATGCCA 509
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 510 TTGAGCCATGTTCTTGGCAACAACTCGGTGCTCGTCTCACCGAGGTTCCGCAAGACGGT 569
Qy 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180

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|||||
Db 570 ACCTGCCCTTGGCTGAGGCTGATGGAGACCCCAAGTCACCGTTGAGTATTACAATGAC 629
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 630 AATGGTGCCAGGGTTCTTATTCGTGTACACACCGCTGAATCTCCACCCCAACACGACGAG 689
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 690 ACTGTCAACCAATGACCAATTTGCTGTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 749
QY 221 ProGluLysThrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 750 CCAGAGAAGTACCTTGTATGAGAAGACCAATTTCCACTCTGAACCCCTTCAGCCGCTTTGTC 809
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThr 260
Db 810 ATTGGTGGCCCTCATGGCATGCTGTCTCACCGGCCGCAAGATCATTTATCGATACTTAT 869
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 870 GGAGGATGGGTGCTCATGTGTGTGTCTTCTCCGGGAAGACCCCTACCAAGGTGTAT 929
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 930 AGGAGTGGTGTACATTTGTGACAGAGGCTGCTAAGAGCATTTGGCAAGTGGACTTGGC 989
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 990 AGAAGGTGCATTTGTGCNAGTGTCTTATGCCATTTGGTGTGCTGAGCCTTTGTCTGTGTT 1049
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1050 GTTGACACCTTATGGCACTGGGAAGATCCATGATGAAGAGATTTCTCAACATTTGTGAAGAA 1109
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1110 AACTTTGATTTACGGCTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAAT 1169
QY 361 AsnArgPheLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1170 AACAGGTTTTTGAAGACTGCTGCTATGGACACTTTTGAAGAGAGAACCCCTGACTTCACA 1229
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1230 TGGGAAGTGTTCANACCCCTCAAGTCGGAGAGGCC 1265
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RESULT 14

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US-10-425-114-8336
; Sequence 8336, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8336
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700748001_FLI
US-10-425-114-8336
Alignment Scores:
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Pred. No.: 3-5e-227 Length: 1458
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservatives: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8336 (1-1458)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 92 ATGGCAGAGACATTCTATTACCTTCAGATCGGTGAACGAGGGACACCTCGACAAGCTC 151
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 152 TCGGACCAAAATCTCGATGTCTCTCGACGCTTGCCCTCGAGCAGACCCGACAGACAAA 211
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 212 GTTGCTCGGAACATGCACCAAAACCAACTTGGTTCATGGTCTTCGGAGAAATCACGACC 271
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 272 AAGGCCAACGTTGACTACGAGAAGATAGTGGGTGCACACTGCAGGAGAACATCGGCTTCGTC 331
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 332 TCAATGATGTGGGACTGGATGCCGACCACTGCAAGGTCTCGTCAACATTGAGCAGCAG 391
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 392 AGCCCTGATATTGCTCAGGGGTGTACACGCGCCACCTTACCAAAAACCTTGAAGAAATGGT 451
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 452 GCTGTGTGACCGGGTGCATGTTGGCTATGTCCTGATGTAAGAACCCCTGAAATTTGATGCCA 511
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 512 TTGAGCCATGTTCTTTGCAACAAAACCTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACCGT 571
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 572 ACCTGCCCTTGGCTGAGGCTGTATGGGAAGACCCCAAGTGACCGTTGAGTATTACAATGAC 631
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 632 AATGGTGCAGGGTTCCTATTGCTGTATCACACCGGTGCTTAATCTCCACCCACACGACGAG 691
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 692 ACTGTCAACCAATGACCAATTTGCTGTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 751
QY 221 ProGluLysThrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 752 CCAGAGAAGTACCTTGTATGAGAAGACCAATTTCCACTCTGAACCCCTTCAGCCGCTTTGTC 811
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrThr 260
Db 812 ATTGGTGGCCCTCATGGCATGCTGTCTCACCGGCCGCAAGATCATTTATCGATACTTAT 871
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 872 GGAGGATGGGTGCTCATGTGTGTGTCTTCTCCGGGAAGACCCCTACCAAGGTGTGAT 931
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
Db 932 AGGAGTGGTGTACATTTGTGACAGCAGGCTGCTAAGAGCATTTGTGGCAAGTGGACTTGGC 991
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 992 AGAAGGTGCATTTGTGCAAGTGTCTTATGCCATTTGGTGTGCTGAGCCCTTTGTCTGTGTTT 1051
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QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1052 GTTGACACCTATGGCACTGGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGGAA 1111
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1112 AACCTTTGATTTCAGGCGTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1171
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1172 AACAGGTTTTGAAGACTGCTGCTATGGACATTTTGGAGAGAGACCCCTGACTTCACA 1231
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1232 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1267

RESULT 15
US-10-425-114-8325
; Sequence 8325, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8325
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700747550_FLI
US-10-425-114-8325

Alignment Scores:
Pred. No.: 3,51e-227 Length: 1461
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8325 (1-1461)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
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QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 155 TGGACCAAAATCTCCGATGCTGCTCGAGCTTGCTCGAGCAGGACCCAGACACACAAA 214
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 215 GTTGCTCGCAACATGCACCAAAACCACTTGGTCATGGTCTTCGAGAAATCAGGACC 274
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 275 AAGGCCAACCGTTGACTACGAGAGATAGTCGTCACACCTGCGAGGAAACATCGGCTTCGTC 334
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 335 TCAATGATGTGGACTGGATGGCACAACCTGCAAGGTCTCTCAACATTGAGAGAGCAG 394
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 1112 GTTGACACCTATGGCACTGGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGGAA 1111
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Db 395 AGCCCTGATATTGCTCAGGGTGTACACGCGCCACCTTACCAAAAAACCTGAGAAATTTGTT 454
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 455 GTTGTGTGACACCGGTTCACATGTTTGGCTATGCGCATGATGAAACCCCTGAAATTGATGCCA 514
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 515 TTGAGCCATGTTCTTTGCAACAAACTCGGTGCTCGTCTCACCGAGGTTCGCAAGAACCGT 574
QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 575 ACTTCCCTTGTGCTGAGGCTGATGGAGAGACCCCAAGTGAACCGTTGAGTATTACATGAC 634
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 635 AATGTTGCCAGGGTTCCTATTCTGCTGACACACCGTCTAATCTCCACCCCAACACGACGAG 694
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 695 ACTGTCAACCAATGACGAAATTCGTCTGACCTCAAAAGAGCATGTGATCAAGCCTGTGATC 754
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 755 CCAGAGAAAGTACCTTGTGATGAGAGAACCAATTTTCCACTTGAACCCCTTCAGGCCGTTTGT 814
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
Db 815 ATTGTGTGCCCTCATGCGGATGCTGCTCTCACCGGCCCGCAAGATCATTATCGATACTTAT 874
QY 261 GlyGlyTrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 875 GGAGGATGGGTGCTCATGCTGGTGGTCTTCTCCGGGAGGACCCCTACCAAGGTTGAT 934
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 935 AGGAGTGGTGTCTTACATTGTGAGACAGGCTGTAAAGAGCAATTGGCAAGTGGACTTGCC 994
QY 301 ArgAspCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 995 AGAAGTGCATTTGTGCAAGTGTCTTATGCCATTGGTGTGCTGAGCCTTTGTCTGTGTTT 1054
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1055 GTTGACACCTATGGCACTGGGAAGATCCATGATAAGAGAGATTCTCAACATTGTGAAGGAA 1114
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1115 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACCTTTGATCTCAAGAGGGGTGGAAT 1174
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1175 AACAGGTTTTGAAGACTGCTGCTATGGACATTTTGGAGAGAGACCCCTGACTTCACA 1234
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1235 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1270
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Search completed: September 12, 2005, 23:19:41
Job time : 875 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2083	100.0	1485	4	US-09-424-9788-38	Sequence 38, Appl
2	1985	95.3	1479	4	US-09-424-9788-40	Sequence 40, Appl
3	1953	93.8	2183	4	US-09-424-9788-37	Sequence 37, Appl
4	1946	93.4	1582	4	US-09-424-9788-35	Sequence 35, Appl
5	1900.5	91.2	1353	4	US-09-424-9788-43	Sequence 43, Appl
6	1891.5	90.8	1380	4	US-09-424-9788-41	Sequence 41, Appl
7	1317.5	63.3	1283	3	US-09-318-448-22	Sequence 22, Appl
8	1317.5	63.3	1283	4	US-09-023-655-1371	Sequence 1371, Ap
9	1317.5	63.3	1283	4	US-09-949-016-4188	Sequence 4188, Ap
10	1317.5	63.3	3495	4	US-09-976-594-470	Sequence 470, App
11	1280.5	61.5	1173	4	US-09-248-796A-4152	Sequence 4152, Ap
12	1274.5	61.2	3320	4	US-09-949-016-1787	Sequence 1787, Ap

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 74 ATGGCAGAGACATCTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTGACAGCTC 133
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 134 TGGGACCAATCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAG 193
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 60
DB 194 GTTGCCCTGGGAAACATGCAACCAAGACCACTGGTCTATGGTCTTCGGAGAGATCACCACC 253
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 254 AAGGCCAAGCTTGACTACGAGAAGATCGTGGTGACACCTGCAGGACACATCGGCTTCGTC 313
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
DB 314 TCAAACGATGTGGGACTTGATGCTGACAACTGCAAGGCTCTGTAAACATTGAGCAGCAG 373
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 374 AGCCCTGATATTGCCCAGGGTGTGACGGCCACCTTACCAAGAGACCCGAGGAATCGGT 433
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 434 GCTGGAGACCGGTCACATGTTTGGCTATGCCAGGACGAACCCCAAGATTGATGCCA 493
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 494 TTGAGTCATGTTCTTGCACACTAACTCGGTGCTCGTCTCACCGAGGTTCCGAAGAACGGA 553
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValClnTyrThrAsnAsp 180
DB 554 ACTGTGCCCATGGTTGAGGCTCTGATGGGAAACCCCAAGTGCATGTTGAGTATTACAAATGAC 613
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 614 AACGGTGCCATGGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCCCAACATGATGAG 673
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 674 ACTGTGACCAACGACGAAATTCGAGCTGACCTCAAGAGCATGTGATCAAGCGGTGATC 733
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 734 CCGGAGAGTACCTTGATGAGAAGACCATTTCCACTTGAACCCCTCTGCGCGTTTGTTC 793
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 794 ATTGGAGGTCTCCACGGTGTGCTGCTCTCACCGGCGCAAGATCATCATGATACTTAC 853
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 854 GGAGGATGGGTGCTCATGCTGGTGTGCTTTCCTCCGGGAGGATCCCAACCAAGGTTGAT 913
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 914 AGAGTGGTGTCTTACATTTGAGACAGGCTGCTAAGAGCATTTGCGAAGTGGACTAGCC 973
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 974 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCCCGAGCCTTTGTCTCTTT 1033
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1034 GTTGACCATATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAG 1093
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1094 AACTTTGATTTTCAAGCCCGGTTATGATCTCATCAACCTTGAATCTCAAGAGGGGTGGGAT 1153
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380

DB 1154 AACAGTTCTTGAAGACTGCTGCATATGACACATTCGGCAGAGAGCCCTGACTTCACA 1213
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAAGGCC 1249
RESULT 2
US-09-424-978B-40
; Sequence 40, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-424-978B-40
Alignment Scores:
Pred. No.: 1e-228 Length: 1479
Score: 1985.00 Matches: 374
Percent Similarity: 97.69% Conservative: 6
Best Local Similarity: 96.14% Mismatches: 9
Query Match: 95.30% Indels: 0
DB: 4 Gaps: 0
US-10-734-698A-39 (1-392) x US-09-424-978B-40 (1-1479)
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DB 123 GAACCTTCTTATTACCTCCGAGTCTGTGACGAGGGTCAACCCAGACAGCTCTGTGAT 182
QY 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
DB 183 CAGATCTCTGATGTCAGTCTTCTTGTGCTGCTTGCAGCAAGATCCGAGAGCAAGTTGCA 242
QY 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
DB 243 TGTGAACCTTCACCAAGACCAACTTGGTCTATGGTCTTTTGGTGAGATCACAACCAAGGCT 302
QY 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
DB 303 ATTGTAGATATGAGAAGATTGCGTGACACATGCCGTATATTTGGATTTTGTCTGAT 362
QY 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 102
DB 363 GATGTTGGTCTTGTGCTGCAACTGCAAGGCTCTTGTTCATTTGAGCAGCAAGTCTCT 422
QY 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyValAlaGly 122
DB 423 GATATTGCTCAAGGTGTCCACGGCCATCTGACCAAAACCCCGAGGAGATTGGTCTGCT 482
QY 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
DB 483 GACCAGGGCCACATGTTGGCTATGCAACACATGAGACCCCTGAATTAAATGCTCTCAGT 542
QY 143 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 162

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Db 543 CACGTGCTTCAACTAACTTGGTCCCGCTTACAGAGCTCCGCAAGAAATGCGACCTGC 602
Qy 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
Db 603 GCCTGGTTGAGGCTGATGCAAGACCAAGTTACTGTTGAGTATAGCAATGAGTGT 662
Qy 183 AlaMetValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrVal 202
Db 663 GCCATGGTTTCAATTAAGGTACACACTGTTCTTATCTCCACCAACACAGATGAGACCGTT 722
Qy 203 ThrAsnAspGluLeuAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 222
Db 723 ACCAATGATGAGATTGCCCGGACCTTAAGAGCATGTCATCAACAGCATCCTCCAGAG 782
Qy 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
Db 783 AAGTACCTTCATGAGAATACTATTTTCCACCTTAACCCATCTGGCCGATTCGTTATTGGT 842
Qy 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 262
Db 843 GGAACCTCATGTGATGCTGCTCACTGGTCTGTAATAATCATCATCGACACTTATGTTGGT 902
Qy 263 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 282
Db 903 TGGGGTGCTCATGTGGTGTGCTTTCTCGGCAAGACCAACCAAGGTCGACAGAGT 962
Qy 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 302
Db 963 GGTGCATACATTGTAAGGCAAGGCTGCAAGAGTATCGTAGCTAGTGGACTTGTCTGTGAC 1022
Qy 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
Db 1023 TGCATCGTGCAGGTATCTTATGCCATCGGTGCTGCTGAGCCATTGCTGTATTGCTGAC 1082
Qy 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
Db 1083 ACCTATGGCACTGGAAGATCCCTGACAGGGAATTTTGAAGATCGTTAAGGAACTTT 1142
Qy 343 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArg 362
Db 1143 GACTTCAGACCTGGAATGATGTCATTAACCTTGAATTTGAAGAGGGTGGCAATAGAAG 1202
Qy 363 PheLeuLysThrAlaLalaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 382
Db 1203 TTCTTGAATACTGCTGCTATGCTGCTACTTTGGACGTGATGACCCCGATTTCATGGGAA 1262
Qy 383 ValValLysProLeuLysTrpGluLys 391
Db 1263 GTTGTCAAGCCCTCAAGTGGGAAAAG 1289

RESULT 3
US-09-424-978B-37
; Sequence 37, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 2183
; TYPE: DNA
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; ORGANISM: Oryza sativa
US-09-424-978B-37
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Pred. No.: 1,34e-224 Length: 2183
Score: 1953.00 Matches: 364
Percent Similarity: 97.11% Conservatives: 14
Best Local Similarity: 93.57% Mismatches: 11
Query Match: 93.76% Indels: 0
DB: 4 Gaps: 0
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US-10-734-698A-39 (1-392) x US-09-424-978B-37 (1-2183)
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Qy 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
Db 860 CAAGTCTCAGATGCTGTGCTTGTATGCTGCTCCGCGAGGACCTGACAGCAAGGTGCT 919
Qy 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
Db 920 TGTGAGACCTGCACCAAGACAAACATGCTCATGCTCTTTGTTGAGATCACCACCAAG 979
Qy 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
Db 980 AACGTTGACTATGAGAAGATTGTCAGGGAGACATGCCGTAAACATCGGTTTGTGTGCT 1039
Qy 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 102
Db 1040 GATGTGGTCTCGATGCTGACCACTGCAAGGTGCTTGTGAACATCGAGCAGGATCCCT 1099
Qy 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 122
Db 1100 GACATTGACAGGTGTGCAAGGCACTTCAACCAAGGCGCTGAGGAGATTGTTGCTGT 1159
Qy 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
Db 1160 GACCAGGACACATGTTGGATGATCACTGATGAGACCCCTGAGTTGATGCCCTCAGC 1219
Qy 143 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 162
Db 1220 CATGTCTTGTACCAAGCTTGGCTGCTCTTACGAGGTTCGCAAGAAATGGGACCTGC 1279
Qy 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
Db 1280 GCATGGCTCAGGCTGACGGGAAGACCCAGTGAATGTTGAGTACCGCAATGAGAGCGT 1339
Qy 183 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 202
Db 1340 GCCAGGTCCTGTCCTGTCACACCGTCTCTCATCTTACCAGCATGATGAGACAGTC 1399
Qy 203 ThrAsnAspGluIleAlaAlaAspLysGluHisValIleLysProValIleProGlu 222
Db 1400 ACCAAGCATGAGATTGCTGTCGCTGAGGAGGAGCATGTCATCAAGCCTGCTATTCC 1459
Qy 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
Db 1460 CAGTACCTTGTATGAGAGACAACTCTTCCATCTTAACCCATCTGTTGCTGCTCAT 1519
Qy 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 262
Db 1520 GGACCTCATGTTGATGCTGCTCTCACTGCGCGAAGATCATCATTTGACACATTTATG 1579
Qy 263 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 282
Db 1580 TGGGAGCTCACGGTGGTGGTCTTCTTCTGCAAGGACCCCAACCAAGGTTGACCGAGT 1639
Qy 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 302
Db 1640 GGAGCATACGTGCGCAAGGCAAGCTGCGCAAGACATTTGTTGTTAGTGGCTTCTGCT 1699
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QY 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
Db 1700 TGCATTGTCCAGTATCATACGCCATCGGTGTCCAGAGCCACTGTCCGTATTGTCTGAC 1759
QY 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
Db 1760 ACATACGGCAGCTGGCAGGATCCCTGACAAAGGAGATCCTCAAGATTGTGAAGGAGAACTTC 1819
QY 343 AppPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArg 362
Db 1820 GACTTCAGGCCCTGGCATGATCATATCAACCTTGACCTCAAGAAAGGGCGCAACGAGCGC 1879
QY 363 PheLeuLysThrAlaIleTyrGlyHisPheGlyValGluAspProAspPheThrTrpGlu 382
Db 1880 TACCTCAAGAGCGCGCTTACGGTCACTTCGGAGAGGAGACCCAGACTTCACCTGGGAG 1939
QY 383 ValValLysProLeuLysTrpGluLys 391
Db 1940 GTGGTGAAGCCCTCAAGTGGGAGAAG 1966
```

RESULT 4

US-09-424-978B-35
; Sequence 35, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; APPLICANT: Abell, Lynne N.

; APPLICANT: Thorpe, Catherine J.

; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes

; FILE REFERENCE: BB-1087

; CURRENT APPLICATION NUMBER: US/09/424,978B

; CURRENT FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: US 60/048,771

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1582

; TYPE: DNA

; ORGANISM: Zea mays

US-09-424-978B-35

Alignment Scores:

Pred. No.:	5,566-224	Length:	1582
Score:	1946.00	Matches:	363
Percent Similarity:	96.92%	Conservative:	14
Best Local Similarity:	93.32%	Mismatches:	12
Query Match:	93.42%	Indels:	0
DB:	4	Gaps:	0

US-10-734-698A-39 (1-392) x US-09-424-978B-35 (1-1582)

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QY 3 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 22
Db 152 GACACCTTCTTCACTCCGAGTGTGTAACGAGGGGACCCCTGACAAGCTCTGCGAC 211
QY 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
Db 212 CAGGTCTCAGATGCCGTCTTTCAGCGCTTGCCTTGTGAGACCCCTGACAGAGGTGTCT 271
QY 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
Db 272 TGTGAGACCTGCACCAAGACCAACATGTTGTCATGGTCTTGTGTGAGATCACCAACGAGGCC 331
QY 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
Db 332 AATGTGACTACGAGAAGATTGTGAGGAGAGCTGCCGCAACATTGGTTTTGTGCAAC 391
QY 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 102
```

```
Db 392 GATGTCCGGCTTGACGCTGACCACTGCAAGGTGCTCGTGAACATTGAGCAGAGTCCCT 451
QY 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 122
Db 452 GATATTGTCTCAGGGTGTGCATGGCCACTTCCCAAGCGCCCCCGAGAGATTGGAGCTGT 511
QY 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
Db 512 GACCAGGACACATGTTCCGGGTATCGGACCGATGAGACCCCTGAGTTGATGCCCTCAGC 571
QY 143 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 162
Db 572 CATGTCCTTGGCACCAACCTAGGTGCTGCTCTCACCAGAGTCCGCAAGACGGAACCTGC 631
QY 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
Db 632 CCTGGCTCAGGCTTGATGGGAAGACCCAGGTGACAGTCCAGTACCGCAATGAGGTTGT 691
QY 183 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 202
Db 692 GCCATGGTCCCCATCCGTGTCCACACCTCTCTCATCTCCACCAGCAGCAGACAGTGT 751
QY 203 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 222
Db 752 ACCAATGATGAGATCGCTGCTGACCTGAAGGAGCATGTCTCATCAAGCCTATCATCCT 811
QY 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
Db 812 CAGTACCTTGGACGAGAACCATCTTCCACCTTAACCCATCCGCCCGCTTTGTCTATTGT 871
QY 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 262
Db 872 GGACCTCAGCGGATGCTGGCTCTACTGGCCGCAAGATCATCATTTGACACCTTACGCT 931
QY 263 TrpGlyAlaHisGlyGlyValAlaPheSerGlyLysAspProThrLysValAspArgSer 282
Db 932 TGGGAGCCCATGGCGTGGCGCTTTCTCCGCAAGGAGACCCCAACCAAGGTTGACCGCAGC 991
QY 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArg 302
Db 992 GGAGCCTATGTGCGAGGAGGAGCTGCCAAGAGCATCGTCGCGCAGCGGCTTTGCTCGCGC 1051
QY 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
Db 1052 GCCATCGTCCAGGTGCTCTACGCCATGCGCGCTGCCGAGCCTCTCTCGTGTGTTGTCAC 1111
QY 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
Db 1112 ACGTAGGCGCACCGCGCGCATCCCGACAAAGAGATCTCTCAAGATTGTCAAGGAGAACTTC 1171
QY 343 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArg 362
Db 1172 GATTTCAGGCTGCGCATGATTATCATCAACCTTGACCTCAAGAAAGGGCGCAACGGGCGC 1231
QY 363 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 382
Db 1232 TACCTCAAGCGCGACCTTACGCCACTTCGGAAGGGAGCAGCCCTGACTTCACTTGGGAG 1291
QY 383 ValValLysProLeuLysTrpGluLys 391
Db 1292 GTGGTGAAGCCACTCAAGTCGGAGAAA 1318
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RESULT 5

US-09-424-978B-43

; Sequence 43, Application US/09424978B

; Patent No. 6664445

; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

```

; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-424-978B-43

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QY 22 AspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysVal 41
Db 139 GACCAAGTCTCCGACCGCGTCTTGGATGCTTGGCCAGAGTCCGACAGCAGGTC 198
QY 42 AlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLys 61
Db 199 GCTCGGACAGCGTCACCAAGACCAACATGGTCTTGGCGGAGATCACCAACAG 258
QY 62 AlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSer 81
Db 259 GCCACCGTCGACTATGAGAAGATCGTGCCTGACACCTGCCGGAACATCGTTCTCT 318
QY 82 AsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSer 101
Db 319 GATGAGTGTGGTCTCGACCGCCAGCCTTGCARGTGCTCGTCAACATCGAGCAGTCC 378
QY 102 ProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAla 121
Db 379 CCTGACATTTGCCAGGCGTTCATGGACACTTCACCAAGCGTCCCGAAGAGTCGGCGC 438
QY 122 GlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 141
Db 439 GGTGACAGGCGATCATGTTGGCTATGCCACCGATGAGACCGCTGAGCTGATGCCCTC 498
QY 142 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 161
Db 499 AAGCAGTGTCTGCCACCAAGCTYGAGCTCGCTCACGAGTCCGCAAGATGCGACC 558
QY 162 CysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsn 181
Db 559 TGGCGCTGGTCCAGGCTCAGCGAAGAGCCAGGTCACAGTCGAGTACCTAAACGAGGAT 618
QY 182 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 201
Db 619 GGTGCCATGCTACCTTCTGTGTGACACCGCTCTCATCTCCACCGACACGACGAGACC 678
QY 202 ValThrAsnAspGluIleAlaLeuLeuLysGluHisValIleLysProValIlePro 221
Db 679 GTACCAACGACGAGATCTCGGACCTCAAGGACATGTCTCAAGCCGGTGATCCCC 738
QY 222 GluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIle 241
Db 739 GCAAAGTACCTCGATGAGAACCACCTCTTCCACCTGAACCGCTCTGGCGCTCGTCATC 798
QY 242 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 261
Db 799 GGCGGCCCCCGGTGACCGCGTCTCACCGCGCGCAAGATCATCATCGACACCTATGCT 858
QY 262 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 281
Db 859 GGTGGGGAGCCACCGCGCGGTGCTCTCTGGCAAGGACCCAAACCAAGTCCGACCGY 918
QY 282 SerGlyValaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301
Db 919 AGTGGCGCTACATGTCAGGCGARGCGCCCAAGAGCATCATCGCCAGCGCGCTCGCACGC 978
QY 302 ArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheVal 321
Db 979 CGCTGCATTTGTGAGATCTCATACGCGCATCGGTGTGCTGAGCGCTTGTGTGTCGTC 1038
QY 322 AspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsn 341
Db 1039 GACTCTACGGCACCGGCAAGATCCCGCAAGAGGAGATCCTCAAGCTCGTGAAGGAGAAC 1098
QY 342 PheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsn 361
Db 1099 TTTGACTTCAGGCGCGGGATGATCAGATCAACCTGGAATTTGAAGAAAGGTGGA--AAC 1155
QY 362 ArgPheLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 381
Db 1156 AGGTTTCATCAAGACCGCTCTTAAGGTCTACTTGGCCGCTGATGATGCCGACTCACCTGG 1215
QY 382 GluValValLysProLeuLysTrpGluLysAla 392
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Db 1216 GAGGTGGTGAAGCCCTCAAGTTCGACAGGCA 1248
RESULT 7
US-09-318-448-22
; Sequence 22, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-22
Alignment Scores:
Pred. No.: 1,97e-148 Length: 1283
Score: 1317.50 Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 3 Gaps: 3
US-10-734-698A-39 (1-392) x US-09-318-448-22 (1-1283)
QY 4 ThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGln 23
Db 114 ACATTCTCTTTTCCACTCAGAGTCGGTCGGGAAGGCCACCAGCAGATAAGATTTGTGACCA 173
QY 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValaLys 43
Db 174 ATCAGTGATGCTGCTCTTGTATGCCCTTTCAGCAGGATCTTGATGCCAAAGATGCTTGT 233
QY 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAACTGTTGTATAAACTGGAATGATCTCTTCTGCTGGGAAATTTACATCCAGAGCTGCT 293
QY 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAAGAGTGGTTCGTGAAGCTGTGTTAAACACATTTGGATATGATGATTTCTTCC 353
QY 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAAGTTTTTGACTCAAGACTTTGTAACGTCTGGTAGCTTGGAGCAACAGTCACAGAT 413
QY 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGT-----CATCTTCACAGAAATGAAGAAGACATTTGGTCTGGAGAC 467
QY 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTTAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGATGCTTTAACCATT 527
QY 144 ValLeuAlaThrLysLeuGlyValaArgLeuThrGluValArgLysAsnGlyThrCysPro 163
Db 528 GTCCTGGGCACCAAGCTAAATGCCAATTCGAGCAACATACGCCCGTAATGGCACTTTGCT 587
QY 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTTCTAAAACTCAAGTTACTGTGTCAGTATATATCAGGATCGAGGTGCT 647
QY 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGTACGACATTTGTTATCTGTTTGTGATGATGATGATGATGATGATGAT 707
```



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Qy 204 AsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTAAAGGAGAAAGTCATCAAGCAGTTGTGGCTGCGAAA 767
Qy 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyGly 243
Db 768 TACCTTGATGAGATACATCTTACCCTACAGCAAGTGGCAGATTGTATTGTGGG 827
Qy 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTyr 263
Db 828 CCTCAGGCTGATCGTTGCTGAGCGGAAATCATTTGTGACACATTTATGCGGTGG 887
Qy 264 GlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGAGGAGTGCTTTTTCAGGAAAGATTATACCAAGGTCGACCGCTTCAGCT 947
Qy 284 AlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgCys 303
Db 948 GCTTATGCTGCTCGTTGGTGCGAAATCCCTTGTAAAGGAGGTCGTGCCGAGGGTT 1007
Qy 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTGTTTCAGTCTCTTATGCTATGAGGTTCTTCATCCATTATCTATCTCCATTTCCAT 1067
Qy 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp 343
Db 1068 TATGGTACCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATTGTGAAGAAGATTTCGAT 1127
Qy 344 PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPhe 363
Db 1128 CTCGCGCTGGGTGCTATGTCAGGGATCTGGATCTGAAGAAG-----CCAATTTAT 1178
Qy 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTyrGluVal 383
Db 1179 CAGAGAGCTCAGCCTATGCGCACTTGTGTAGGAC-----AGCTTCCATGCGAAGTG 1232
Qy 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCAAAAAGCTTAAATATTGAAAG 1256

RESULT 8
US-09-023-655-1371
; Sequence 1371, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
```

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; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1371:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g36326
; US-09-023-655-1371

Alignment Scores:
Pred. No.: 1,97e-148 Length: 1283
Score: 1317.50 Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 4 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-023-655-1371 (1-1283)
Qy 4 ThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuLysAspGln 23
Db 114 ACATTCCTTTTTCACCTCAGAGTCGTCGCGGAGGCCACCCAGATAGATTGTGACCAA 173
Qy 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCys 43
Db 174 ATCAGTGATGCTGCTCTTGTATGCCACCTTACGACAGGATCCTGATGCCAAAGTAGCTGT 233
Qy 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAACTGTTGTCTAAACTGGAATGATCTCTTCTGCTGGGAAATTTACATCCAGAGCTGT 293
Qy 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAGAAAGTGTGTCGTAAGCTGTTAAACACATTTGGATATGATGATTCTTCC 353
Qy 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAAAGTTTGTACTACAAGACTTGTAACTGCTGTGTGTAGCTTTGGAGCAACAGTCACCAT 413
Qy 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGTT-----CATCTTGACAGAAATGAAGAAGCATTTGGTCTCGAGAC 467
Qy 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTAAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCTTTTACCATT 527
Qy 144 ValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysPro 163
Db 528 GTCTTGGCACACAGCTAAATGCCAACTAGCCAGAACTAGCCCGTAATGGCACTTTGCT 587
Qy 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTCTTAAACTCAAGTTACTGTGCGAGTATATCGAGGATCGAGTGT 647
Qy 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGAGTCCACAAATTTATATCTGTTTACGATGATGAGAGGTTTGT 707
Qy 204 AsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTAAAGGAGAAAGTCATCAAGCAGTTGTGGCTGCGAAA 767
Qy 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyGly 243
Db 768 TACCTTGATGAGATACATCTTACCACCTACAGCAAGTGGCAGATTGTATTGTGGG 827
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QY 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTrp 263
Db 828 CCTCAGGGTGATGCTGGTTGATCTGGACCGGAAATCAITGTGGACACTTATGGCGGTGG 887
QY 264 GlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGGAGGAGTCCCTTTTCAGGAAGGATTATACCAAGGTCGACCGTTCAGCT 947
QY 284 AlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCys 303
Db 948 GCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTGTAAAGAGGCTGTCGCCGAGGGTT 1007
QY 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTTGTTCAAGTCTCTTATGCTATGGAGTTTCTCATCCATTATCATCTCCATTTTCCAT 1067
QY 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp 343
Db 1068 TATGGTACCTTCAGAAGAGTGGAGAGAGCTATTAGAGATTGTGAAGAAGAAATTCGAT 1127
QY 344 PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArgPhe 363
Db 1128 CTCGCCCTGGGGTCAATTGCTGGGATCTGGATCTGAAGAG-----CCAATTAT 1178
QY 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluVal 383
Db 1179 CAGAGACTGCAGCTATGGCCACTTGTAGGAC-----AGCTTCCATGGGAAGTG 1232
QY 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCMAAAGCTTAAATATTGAAG 1256
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RESULT 9

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US-09-949-016-4188
; Sequence 4188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4188
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4188
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Alignment Scores:
Pred. No.: 1283
Score: 1317.50 Length: 1283
Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 4 Gaps: 3
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US-10-734-698A-39 (1-392) x US-09-949-016-4188 (1-1283)

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QY 4 ThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGln 23
Db 114 ACATTCTTTTTCACCTCAGAGTCGGTCGGGAAGGCCACCCAGATAAGATTTGTGACCAA 173
QY 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCys 43
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Db 174 ATCAGTGATGCTGCTTGTATGCCACCTTCAGCAGGATCCTGATGCCAAGTAGCTGTGT 233
QY 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAAACTGTGTGCTAAACACTGGAATCATCTTCTGCTGGGAAATATACATCCAGAGCTGT 293
QY 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAAGAGTGGTTGCGAAGCTGTTAAACACATTTGGATATGATGATTCTTCCC 353
QY 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAGGTTTTGACTACAGACTTGTAACTGCTGGTAGCTTGGAGCAACAGTCCACCAGAT 413
QY 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGTT-----CATCTTCACAGAAATGAAGAAGACATTGCTGCTGGAGAC 467
QY 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTTAATGTTTGGCTATGCCACTGATGAAACTGAGGAGTGTATGCTTTAACCAATT 527
QY 144 ValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValAlaArgLysAsnGlyThrCysPro 163
Db 528 GTCTTGGCACAACAAGCTAAATGCCAACTGGCAGAACTACGCCGTAAATGGCAGCTTGGCT 587
QY 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTCTAAAACTCAAGTTACTGTGCAGTATATGCAGGATCGAGGTGCT 647
QY 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGAGTCCACAAATTTGTTATCTGTTACGATGATGAAGAGGTTTGT 707
QY 204 AsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTTAAAGGAGAAAGTCATCAAAAGCAGTTGTGCTCGCAAA 767
QY 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyLys 243
Db 768 TACCTTGATGAGGATACAAATCTACCACCTACAGCCAAGTGCAGATTTGTTATTGCTGGG 827
QY 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTrp 263
Db 828 CCTCAGGGTGATGCTGGTTTACCTGGACGCAAAATCATTTGTGGACACTTATGGCGGTGG 887
QY 264 GlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGGAGGAGTGCCTTTTCAGGAAGGATTATACCAAGGTCGACCGTTCAGCT 947
QY 284 AlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCys 303
Db 948 GCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTGTAAAGAGGAGTCTGTCGCCGAGGGTT 1007
QY 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTTGTTCAAGTCTCTTATGCTATGGAGTTTCTCATCCATTATCATCTCCATTTTCCAT 1067
QY 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp 343
Db 1068 TATGGTACCTTCAGAAGAGTGGAGAGAGCTATTAGAGATTGTGAAGAAGAAATTTCCAT 1127
QY 344 PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArgPhe 363
Db 1128 CTCGCCCTGGGGTCAATTGCTGGGATCTGGATCTGAAGAG-----CCAATTAT 1178
QY 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluVal 383
Db 1179 CAGAGACTGCAGCTATGGCCACTTGTAGGAC-----AGCTTCCATGGGAAGTG 1232
QY 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCMAAAGCTTAAATATTGAAG 1256
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Db	637	TGGTTACGCCCTGANTCTAAACATCAAGTTACTGTGTCAGTATATGCAAGGATCAGAGTGCT	636
Qy	184	MetValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrValThr	203
Db	697	GTGCTTCCCATCAGAGTCCACACAATGTTTATATCTGTTCAGCATGATGAAGAGGTTTGT	756
Qy	204	AsnAspGluLeuLeuAlaAlaAspLeuLysGluHisValleLysProValIleProGluLys	223
Db	757	CTTGATGAAATGAGGATGTCCTTAAAGGAGAAAGTATCAAAAGCAGTTGTGCTCGCGAAA	816
Qy	224	TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyVArgPheValIleGlyGly	243
Db	817	TACCTTGATGAGGATACAACTCTACCACTACACCAAGTGGCAGATTGTATTGTGGGG	876
Qy	244	ProHisGlyAspAlaGlyLeuThrGlyVArgLysIleIleLeuAspThrTyrGlyGlyTrp	263
Db	877	CCTCAGGTCATGCTGGTTTGACTGGACGGGAAATCATTTGTGCACACTTATGCGGTTGG	936
Qy	264	GlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly	283
Db	937	GGTGCTCATGAGGAGGTGCTTTTCAGGAAAGGATTATACCAAGGTTCGACCGTTTCAGCT	996
Qy	284	AlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgCys	303
Db	997	GCATTATGCTGCTCGTTGGTGGGCAAAATCCCTTTTAAAGGAGGTCTGTGCCCGGAGGTT	1056
Qy	304	IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr	323
Db	1057	CTTGTTTCAGGTCTCTTATGCTATTGGAGTTTCTCATCCATTATCTATCTCCATTTTCCAT	1116
Qy	324	TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp	343
Db	1117	TATGGTACCTCTCAGAAGAGTGAAGAGAGCTATTAGAGATTGTGAAGAAGATTTCGAT	1176
Qy	344	PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPhe	363
Db	1177	CTCCGCCCTGGGTGCATTGTGAGGATCTGGATCTGAAGAAG-----CCAATTTAT	1227
Qy	364	LeuLysThrAlaAlaTyrGlyHisPheGlyVArgGluAspProAspPheThrTrpGluVal	383
Db	1228	CAGAGGACTGCACCTATGGCCACTTTGGTAGGGAC-----AGCTTCCCATGGGAAGTG	1281
Qy	384	ValLysProLeuLysTrpGluLys	391
Db	1282	CCCAAAAGGCTTAATATTATTAAG	1305
RESULT 11			
US-09-248-796A-4152			
; Sequence 4152, Application US/09248796A			
; Patent No. 6747137			
; GENERAL INFORMATION:			
; APPLICANT: Keith Weinstock et al			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA			
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: 107196.132			
; CURRENT APPLICATION NUMBER: US/09/248,796A			
; CURRENT FILING DATE: 1999-02-12			
; PRIOR APPLICATION NUMBER: US 60/074,725			
; PRIOR FILING DATE: 1998-02-13			
; PRIOR APPLICATION NUMBER: US 60/096,409			
; PRIOR FILING DATE: 1998-08-13			
; NUMBER OF SEQ ID NOS: 28208			
; SEQ ID NO 4152			
; LENGTH: 1173			
; TYPE: DNA			
; ORGANISM: Candida albicans			
US-09-248-796A-4152			
Alignment Scores:			
Pred. No.:		4,88e-144	Length: 1173
Score:		1280.50	Matches: 242
Percent Similarity:		77.00%	Conservative: 56
Best Local Similarity:		62.53%	Mismatches: 82


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Db 477 GGTGGTGGTTCGGCTATGCTACCGACGACGACGAGGTGCATGCCCTCCACCATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTyrP 164
Db 537 CTGTGCTCACAGCTCAACGCCCGATGGCAGACCTCAGGGCTCCGGCTCTCCCTCCCTGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGCGGCTGACTCTAAGACTCAGGTGACAGTTTCAATGATGACGACCAATGGCGAGTC 656
Qy 185 ValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCTCTGTGCGACGACCAAGACATCATCGCTG 716
Qy 205 AspGluAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGAGATGCGCAGGCGCTTGAAGGCAAGTATCATCGGGCGCTGGTGGCGCCAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGGACGAAGACACCGTCTACCCCTGCAGCCCGCTGAGTGGGCGCTTGTCTATCGAGGTGCC 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyTyrGly 264
Db 837 CAGGGGATGCGGGTGTCTACCTGGCCCTGATGATTTATGTCAGACCATGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTGTGGGGCTTCTCTGGGAAGGACTACACCAAGGTGGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCysIle 304
Db 957 TATGCTGCCGCTGGGTGGCCAACTCTGTGTGAAGCAGGGCTCTGCGGAGAGTGT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
Db 1017 GTCCAGGTTTCTATCCATGTTGTGGCGGCGCTGCTGCTATTCATCTTCCACCTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGAACCTCTCAGNAGACAGCGAGCTGTGGATGTGTGATGAATAAGACTTCGACCTC 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCGCGGCGCTATTCAGGGATTTGGACTTGAAGAAG-----CCCATCTACCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTyrGluValVal 384
Db 1188 AAGACAGCATGCTATGGCCATTTCCGAAGAAGC-----GAGTTCCCATGGGAGGTGCC 1241
Qy 385 LysProLeu 387
Db 1242 AGNAGCTT 1250

RESULT 13
US-09-318-448-20
; Sequence 20, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-20
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Alignment Scores:

Pred. No.: 1.32e-142 Length: 3228
Score: 1274.50 Matches: 241
Percent Similarity: 78.85% Conservative: 61
Best Local Similarity: 62.92% Mismatches: 74
Query Match: 61.19% Indels: 7
DB: 3 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-318-448-20 (1-3228)

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Qy 5 PheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGlnIle 24
Db 123 TTTCATGTTTCACATCGGAGTCTGTGGGAGAGGACACCCGGATAAAGATCTGTACCAGATC 182
Qy 25 SerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCysGlu 44
Db 193 AGTGATGACAGTCTGGATGCCCATCTCAAGCAGACCCCNATGCCNAGGTGGCTGTGAG 242
Qy 45 ThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnVal 64
Db 243 ACAGTGTGCAAGACCGGCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
Qy 65 AspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAspVal 84
Db 303 GACTACCAAGCGGTGTGAGGACACCATCAAGCACATCGGCTACGATGACTCAGCCAAAG 362
Qy 85 GlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIle 104
Db 363 GCTTTGATCTTCAGACTTCGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
Qy 105 AlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAspGln 124
Db 423 GCCCAGTGGCTC-----CATCTGCACAGAAATAGGAGGATGTGGGGCAGGAGATCAG 476
Qy 125 GlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisVal 144
Db 477 GGTTTGATGTTTGGGTATGTATCCGACGACGACGAGGAGTGCATCCCTCCACCATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTyrP 164
Db 537 CTGTGCTCACAGCTCAACGCCCGATGGCAGACCTCAGGGCTCCGGCTCTCCCTCCCTGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGCGGCTGACTCTAAGACTCAGGTGACAGTTTCAATGATGACGACCAATGGCGAGTC 656
Qy 185 ValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCTCTGTGCGACGACCAAGACATCATCGCTG 716
Qy 205 AspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGAGATGCGCAGGCGCTTGAAGGCAAGTATCATCGGGCGCTGGTGGCGCCAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGGACGAAGACACCGTCTACCCCTGCAGCCCGCTGAGTGGGCGCTTGTCTATCGAGGTGCC 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyTyrGly 264
Db 837 CAGGGGATGCGGGTGTCTACCTGGCCCTGATGATTTATGTCAGACCATGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTGTGGGGCTTCTCTGGGAAGGACTACACCAAGGTGGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCysIle 304
Db 957 TATGCTGCCGCTGGGTGGCCAAAGTCTGTGTGAAGCAGGGCTCTGCGGAGAGTGT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
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Db 1017 GTCCAGGTTTCTATGCCATTGGTGGCCGAGCGCTGTCATTTCCATCTTCCACTTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGAACCTCTCAGAAGACAGAGCGAGAGCTGCTGGATGTGGTCATGAAGAATTCGACCTC 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCCCGGGCGTCAATGTCAGGGAATTTGGACTTGAAGAAG-----CCCATCTACCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValVal 384
Db 1188 AAGACAGCATGCTACGGCCATTTCGGAAGAAGC-----GAGTTCCCATGGGAGGTTC 1241
Qy 385 LysProLeu 387
Db 1242 AGGAAGCTT 1250

RESULT 14
US-09-949-016-68
; Sequence 68, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-68

Alignment Scores:
Pred. No.: 1,32e-142 Length: 3228
Score: 1274.50 Matches: 241
Percent Similarity: 78.85% Conservative: 61
Best Local Similarity: 62.92% Mismatches: 74
Query Match: 61.19% Indels: 7
DB: 4 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-949-016-68 (1-3228)
Qy 5 PheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGlnIle 24
Db 123 TTCATGTTTACATCGGAGTCTGTGGAGAGGGACACCCCGGATAAGATCTGTGACCCAGTC 182
Qy 25 SerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCysGlu 44
Db 183 AGTGATGCAGTGTGGATGCCATCTCAAGCAAGACCCCAATGCCAAGGTGGCTGTGAG 242
Qy 45 ThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnVal 64
Db 243 ACAGTGTGCAAGACCGGCGATGCTGTGTGTGGATGATCACCTCAATGGCCATGGTG 302
Qy 65 AspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAspVal 84
Db 303 GACTACACGGGTGTGGAGGACACCATCAAGCACATCGGTACGATGACTGACGCAAG 362
Qy 85 GlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerProAspPhe 104
Db 363 GGCTTTGACTTCAAGACTTTCGAACGTGCTGGTGTGGCTTTTGGAGCAGCAATCCCCAGATAT 422
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Qy 105 AlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyValAlaGlyAspGln 124
Db 423 GCCCAGTCCGTC-----CATCTGGACAAATAGGAGGATGTGGGGCGAGAGATCAG 476
Qy 125 GlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisVal 144
Db 477 GGTTTGATGTTTGGCTATGCTACCGACGAGACAGAGGAGTGCATGCCCTCACCATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTrp 164
Db 537 CTGTGTCACAAAGCTCAACGCCCGGATGGCAGACCTCAGCGCTCCGGCTCTCCCTCCCTGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGGGCTGACTCTNAGACTCAGGTGACGTTTCTAGTACATGCAGACACANTGGCCGAGTC 656
Qy 185 ValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCGTCATCTCTGTGCAGACACAACGAAGACATCAGCGTG 716
Qy 205 AspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGATATGCGCAGCGGCCCTGAAGGAGCAAGTCTATCAGGGCGGTGGTCCCGGCCAAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGACGAAAGACACCGTCTACCTCGACGCCAGTGGCGGTGTGTCTATCGAGGTCCC 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyLysTrpGly 264
Db 837 CAGGGGATGCGGGTGTCACTGGCCGTAAGATTATTGGGACACCCTATGGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTTGGTGGGGCTTCTCTGGGAAGGACTACACCAAGGTAGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgCysIle 304
Db 957 TATGTCGCCCGCTGGTGGCCAGTCTCTGTGTGAAGCAGGGCTCTGCGGAGAGTGCTT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
Db 1017 GTCCAGGTTTCTATGCCATTGGTGGCCGAGCGCTGTCATTTCCATCTTCCACTTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGAACCTCTCAGAAGACAGAGCGAGAGCTGTGGATGTGGTGCATAGAAGCTTCGACCTC 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCCCGGGCGTCAATGTCAGGGAATTTGGACTTGAAGAAG-----CCCATCTACCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValVal 384
Db 1188 AAGACAGCATGCTACGGCCATTTCGGAAGAAGC-----GAGTTCCCATGGGAGGTTC 1241
Qy 385 LysProLeu 387
Db 1242 AGGAAGCTT 1250

RESULT 15
US-09-107-532A-3167
; Sequence 3167, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
```

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STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATON NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3167:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1215
SEQUENCE DESCRIPTION: SEQ ID NO: 3167:
US-09-107-532A-3167

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Alignment Scores:
Pred. No.: 1.63e-122 Length: 1215
Score: 1102.00 Matches: 223
Percent Similarity: 72.56% Conservative: 60
Best Local Similarity: 57.18% Mismatches: 93
Query Match: 52.90% Indels: 14
DB: 4 Gaps: 5

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US-10-734-698A-39 (1-392) x US-09-107-532A-3167 (1-1215)

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QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAsp---Lys 19
DB 19 ATGGTAGAAGACACATTTATTACATCAGATCTGTTCTGAAAGACATCCACGTATATAA 78
QY 20 LeuCysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSer 39
DB 79 ATTGCTGACCAAAATCAGTGATGCAATCTTGATGCAATTTTAAACAAGATCCACAGCA 138
QY 40 LysValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 59
DB 139 CGAGTAGCGGTGGAACGCTCTGTAACAACTTGTGTTTGTAGTATTTGGAGAAATATCT 198
QY 60 ThrLysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPhe 79
DB 199 ACCAGCGCATATGTAGATATTCAAAAGTGTACGGGAACAATAAAGAAATTTGTTAT 258
QY 80 ValSerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 99
DB 259 ACAGTGCAAAATTCGGATTGATGGAGATACAGCAGCTGTATTGGTTGGATTGATGAA 318
QY 100 GlnSerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGlu----- 117
DB 319 CAATCTCCTGATATTGCTCAAGGAGTTGATGAAGCATTGAGATCCGGATGAAGATAAA 378

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QY 118 -----GluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAlaThr 132
DB 379 AAAGACGTATTAGATGAGATTGGTCTGTGACCAAGGTTTAATGTTTGGTTCGTGTA 438
QY 133 AspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAlaArg 152
DB 439 GATGAAACACCAAGATTGATGCTTTTACCAATCGCTTTCAGTCATCGTGGTACGACGC 498
QY 153 LeuThrGluValArgLysAsnGlyThrCysProTyrLeuArgProAspGlyLysThrGln 172
DB 499 TTGGCAGATTTCGTAAATCAATGAAATTAACGTATTACGTCAGATCCAAAATCTCAA 558
QY 173 ValThrValGluTyrTyrAsnAspAsnGlyAlaMetValProValArgValHisThrVal 192
DB 559 GTAACGGTTGAA---TATGATGATCAAGACAA-----CCGGAACCGCTAGATACAATC 609
QY 193 LeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLeuLys 212
DB 610 GTTATTTCAACACAGCATGATGATGAGTAGATAATGAACAATTCGTGATGATCATC 669
QY 213 GluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePheHis 232
DB 670 GAAAAGTAGTGAAGAGTTATTCAGCTGAATATTAGATGATCAACAGAAATATTAT 729
QY 233 LeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuThrGly 252
DB 730 ATCAATCCGACTGGCGGATTTCATTTGGTCTCCTCAAGGGGATCCCGGATTAACAGGA 789
QY 253 ArgLysIleIleAspThrTyrGlyGlyTyrGlyAlaHisGlyGlyGlyValAlaPheSer 272
DB 790 AGAAAAATCATTTGTTGATACGTTATGCGGTTATGCTGCTGCTGGTGGCGGCTTTTCT 849
QY 273 GlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaLys 292
DB 850 GGTAAAGATGCCACAAAGTTGACGTTCTGCCAGCTATGCTGCAGCTTATATTGCTAAA 909
QY 293 SerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaIleGly 312
DB 910 AACATTGTTGCAGCAGGGCTTGCTGCCAAAGCAGAAAGTACAGCTAGCTATTCGATTGGT 969
QY 313 ValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAspLys 332
DB 970 GTTGTCAACCTGTTTCGATCTCAATCAATACTTTTCGGTACTTGGAAACGGTTCGGAAGAA 1029
QY 333 GluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIleAsn 352
DB 1030 GAACGTATTGCTGAGTGAGAGAAAACCTTCGATCTTCGGCCAGCAGGATCATCGAGATG 1089
QY 353 LeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHisPhe 372
DB 1090 CTTGATTTGCGTCGT-----CCGATTTTCAAAACAACAGCTGCTTACGTCATTTT 1140
QY 373 GlyArgGluAspProAspPheThrTrpGlu 382
DB 1141 GGTCTGACAGATGTAGATTTCCTTTGGGAA 1170

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